

Other ESTs: EST06373
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13 Reverse.

```

Location/Qualifiers
1. .357
/organism="Homo sapiens"
/db_xref="ATCC (inhost):85007"
/db_xref="taxon:9606"
/clône="HIBBE91"
/clone lib="Infant Brain, Bento Soares"

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90 a 107 c 96 g 61 t 3 others

Query Match 8.9%; Score 248.6; DB 145; Length 357;
Best Local Similarity 83.1%; Pred. No. 3.7e-47;
Matches 281; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

[illegible]

F11702 340 bp mRNA EST 12-MAR-1995
HSC30E051 normalized infant brain cDNA Homo sapiens cDNA clone
c-30e05, mRNA sequence.

F11702.1 GI:706008

huma

Homo s

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 340)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Deviglieri, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.

M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenz, P., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.

Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, J.,
Sebastiani-Kabaktchis, C. and Tessier, A. . . . of the human genome

Sebastiani-Kabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
and its expression

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and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

C. R. Acad. Sci. III, Sci. Vie 316 (27, 205-272 (1997),
95277534

95277534
Contact: Genethon

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Genethon Centre de recherche sur le Genome Humain
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1, rue de l'Internationale, BP00 51002 EVRY CEDEX,
Tel: 33169472800

MEDLINE
COMMENT

FEATURES
source

BASE COUNT	75 a	83 c	90 g	47 t	6 others
ORIGIN					

Query Match 8.2%; Score 228.4; DB 140; Length 301;
Best Local Similarity 84.3%; Pred. No. 1.7e-42;
Matches 253; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy	893	ggcgatctcacctgtgggggtgtgcaccctggagctggggagcaccgaggtcctgctggac	952
Db	1	GGGGACCTCACCTGTGGGGTCTGTGCCCTGGAGCTAGGGAGCACNGAGGTGCTACTGGAC	60
Qy	953	cacctcaagtctcacgcggaagaaaaggccaaccaggcaccaggggagaagaaataccag	1012
Db	61	CGNNTCNNAGCCCATGCGGAAGAGAAGCCCCCTAGCGGANCCAAGGAAAAGAAGCACCAG	120
Qy	1013	tgcgaccactgtgatagatgcttctacaccggaaagatgtgcgctcgccacctgggtggtc	1072
Db	121	TGCGACCACTGTGAAAGATGCTTCTACACCCGGAAGGATGTGCGACGCCACCTGGTGGTC	180
Qy	1073	cacacaggatgcaaggacttcctgtgtcagttctgtgccagagatttgggcgcaaagac	1132
Db	181	CACACAGGATGCAAGGACTTCCTGTGCCAGTTCTGTGCCAGAGATTGGGCGCAAGGTT	240
Qy	1133	cacctcactcgtcacaccaagaagaccactcccaggagctgatgcaagagaatatgcag	1192
Db	241	CACCTCACCCGGCATAACCAAGAAGACCCACTCACAGGAGCTGATGAAAGAGAGCTTGCAG	300

RESULT 15
F08789

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F08789
LOCUS          F08789          290 bp      mRNA          EST          20-FEB-1995
DEFINITION    HSC2AH041 normalized infant brain cDNA Homo sapiens cDNA clone
               c-2ah04, mRNA sequence.
ACCESSION     F08789
VERSION       F08789.1  GI:673259
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 290)
AUTHORS       Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes
               ,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
               Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
               Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE         IMAGE: molecular integration of the analysis of the human genome

```

and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr

FEATURES
source

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Location/Qualifiers
1. .290
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-2ah04"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain
; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

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BASE COUNT
ORIGIN

Bento Soares, P.N.A.S in press

Query Match 8.1%; Score 226.2; DB 140; Length 290;
Best Local Similarity 85.9%; Pred. No. 5.4e-42;
Matches 249; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

		Matches	2497	CONSERVED	
Qy	893	ggcgatctcacctgtg	gggggtgtgcaccctggagctggggagcaccgaggtcctgctggac	952	
Db	1	GGGGACCTCACCTGTG	GGGGTCTGTGCCCTGGAGCTAGGGAGCACNGAGGTGCTACTGGAC	60	
Qy	953	cacctcaagtctcacgcggaagaaaaggccaaccaggc	acccagggagaagaaataccag	1012	
Db	61	CANTTCAAAGCCCATGC	GGAAGAGAAGCCCCCTAGCGGANCCAAGGAAAAGAAGCACCAG	120	
Qy	1013	tgcgaccactgtgatagatgcttctacacccgaaagatgtgcgtcgccacctggtggtc		1072	
Db	121	TGCGACCACTGTGAAAGATGCTTCTACACCCGGAAGGATGTGCGACGCCACCTGGTGGTC		180	
Qy	1073	cacacaggatgcaaggacttcctgtgtcagttctgtgccagagatttgggcgcaaagac		1132	
Db	181	CACACAGGATGCAAGGACTTCCTGTGCCAGTTCTGTGCCAGAGATTGGGCGCAAGGTT		240	
Qy	1133	cacctcactcgtcacaccaagaagacccactcccaggagctgatgcaaga		1182	
Db	241	CACCTCACCCGGCATA	CCAAGAAGACCCACTCACAGGAGCTGATGAAAGA	290	

Db 993 CCAGGGAGAAGAAATACCAAGTGCGACCACTGTGATAGATGCTTCTACACCCGAAAGATG 1052
 Qy 1314 tgcgacgccacctggtggtccacacaggatgcaaggacttcctgtgccagttctgtgccc 1373
 Db 1053 TCGGTCGCCACCTGGTGGTCCACACAGGATGCAAGGACTTCCTGTGTCAAGTTCTGTGCCC 1112
 Qy 1374 agagatttgggcgcaaggatcacctcaccggcgataccaagaagaccactcacaggagc 1433
 Db 1113 AGAGATTGGGCGCAAAGACCACCTCACTCGTCACACCAAGAAGACCCACTCCCAGGAGC 1172
 Qy 1434 tgatgaaagagagcttgagaccggagaccttctgagcaccttccacaccatctcgccctt 1493
 Db 1173 TGATGCAAGAGAATATGCAGGCAGGAGATTACCAGAGCAATTTCCAACCTCATTGCGCCTT 1232
 Qy 1494 ca-----ttccaactgaaggctgctgccttgccctcctttcccttttaggagcttctgccc 1547
 Db 1233 CAACTTCGTTCCAGATAAAGGTTGATCCCATGCCTCCTTTCCAGCTAGGAGCGGCTCCCG 1292
 Qy 1548 agaacgggcttgcaagtagcttgccagctgaggtccatagcctcaccctcagtcccccag 1607
 Db 1293 AGAACGGGCTTGATGGTGGCTTGCCACCCGAGGTTTCATGGTCTAGTGCTTGCTGCCCCAG 1352
 Qy 1608 aacaagccgcccagcctatgcagccgctg 1636
 Db 1353 AAGAAGCTCCCCAACCCATGCCGCCCTTG 1381

Qy	1	MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPDGKAFVSRYKLMRHMATHSPQK	60
Db	1	MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPDGKAFVSRYKLMRHMATHSPQK	60
Qy	61	SHQCAHCEKTFNRKDHLKNHLQTHDPNKMAFGCEECGKKYNTMLGYKRHLALHAASSGDL	120
Db	61	SHQCAHCEKTFNRKDHLKNHFQTHDPNKMAFGCEECGKKYNTMLGYKRHLALHAASSGDL	120
Qy	121	TCGVCALELGSTEVLLDHLKAHAEEKPPSGTKEKKHQCDHCERC FYTRKDVRRHLVVHTG	180
Db	121	TCGVCALELGSTEVLLDHLKAHAEEKPPSGTKEKKHQCDHCERC FYTRKDVRRHLVVHTG	180
Qy	181	CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTGDLLSTFHTISPSFQLKAAALP	240
Db	181	CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTGDLLSTFHTISPSFQLKAAALP	240
Qy	241	PFPLGASAQNGLASSLPAEVHSLTSPPEQAAQPMQPLPESLASLHPSVSPGSPPPPLPN	300
Db	241	PFPLGASAQNGLASSLPAEVHSLTSPPEQAAQPMQPLPESLASLHPSVSPGSPPPPLPN	300
Qy	301	HKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDLAKGNAGKVN	360
Db	301	HKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDLAKGNAGKVN	360
Qy	361	LPKELPADAVNLTIPASLDLSPLLGFWQLPPPATQNTFGNSTLALGPGESLPHRLSCLGQ	420
Db	361	LPKELPADAVNLTIPASLDLSPLLGFWQLPPPATQNTFGNSTLALGPGESLPHRLSCLGQ	420
Qy	421	QQQEPPLAMGTVSLGQLPLPPIPHVFSAGTGSAILPHFHHAFR	463
Db	421	QQQEPPLAMGTVSLGQLPLPPIPHVFSAGTGSAILPHFHHAFR	463

RESULT 5

P70616

ID P70616 PRELIMINARY; PRT; 583 AA.
AC P70616;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE LOT1.
GN LOT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=97294608; PubMed=9150364;
RA Abdollahi A., Roberts D., Godwin A.K., Schultz D.C., Sonoda G.,
RA Testa J.R., Hamilton T.C.;
RT "Identification of a zinc-finger gene at 6q25: a chromosomal region
RT implicated in development of many solid tumors.";
RL Oncogene 14:1973-1979(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=97301600; PubMed=9158001;
RA Abdollahi A., Godwin A.K., Miller P.D., Getts L.A., Schultz D.C.,
RA Taguchi T., Testa J.R., Hamilton T.C.;
RT "Identification of a gene containing zinc-finger motifs based on lost
RT expression in malignantly transformed rat ovarian surface epithelial
RT cells.";
RL Cancer Res. 57:2029-2034(1997).
DR EMBL; U72620; AAB67042.1; -.
DR HSSP; P03001; 1TF3.
DR INTERPRO; IPR000822; -.
DR PFAM; PF00096; zf-C2H2; 7.
DR PRINTS; PR00048; ZINCFINGER.
DR PROSITE; PS00028; ZINC FINGER C2H2; 7.
KW Zinc-finger; Metal-binding; DNA-binding.
SQ SEQUENCE 583 AA; 65960 MW; 8501071AADFB3F4B CRC64;

Query Match 70.1%; Score 1763; DB 11; Length 583;
Best Local Similarity 56.6%; Pred. No. 1.6e-135;
Matches 330; Conservative 49; Mismatches 84; Indels 120; Gaps 4;

QY 1 MATFPCQLCGKTFLTLEKFTIHNYSHSRERPYKCVQPCGKAFVSRYSKLMRHMATHSPQK 60
Db 1 MAPFRCQKCGKSFLTLEKFTIHNYSHTRERPFKCSKTECGKAFVSKYKLMRHMATHSPQK 60
QY 61 SHQCAHCEKTFNRKDHLKKNHLQTHDPNKMAFGCEECKKYNMGLGYKRHLALHAASSGDL 120
Db 61 THQCTHCEKTFNRKDHLKKNHLQTHDPNKMIYACEDCGKKYHTMGLGYKRHMALHSASSGDL 120
QY 121 TCGVCALELGGSTEVLDDHLKAHAEEKPPSGTKEKKHQCDHCERCIFYTRKDVRRHLVVHTG 180
Db 121 TCGVCTLELGGSTEVLDDHLKSHAEEKAHAPREKKHQCDHCERCIFYTRKDVRRHLVVHTG 180
QY 181 CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMKESLQTGDLSTFHTISPSFQLKAAALP 240
Db 181 CKDFLCQFCAQRFGRKDHLTRHTKKTHSQELMQESLQAGEYQGGYQPIAPPFQIKADPMP 240
QY 241 PFPLGASAQNGGLASSLP AEVHSLTSLPPEQAAQ-----PMQPLPESLASLHPSVSPGSP 294
Db 241 PFQLEMPPEGLDGGGLPPEIHGLVLASPEEVPQPMLSMPMPQMPPEQPTLHPGVVPSSP 300
QY 295 PP-PLPNHKYNTTSTSYSPLASLPLKADTKGFCNISLFEDLPLQEPQSPQKLNPGFDLAK 353
Db 301 PPIILQEHKYSVPVTSFAPFVSMMPKADLKGFCNMGLFEEFPLQECQSPVKFSQCFEMAK 360
QY 354 GNAGKVNLPKELPADAVNLTIPASLDLSPLLGFQWQLPPPATQNTFGNSTLALGPGESLPH 413
Db 361 EGFGKVTLPKELLVDAVNIAIPGSLEISSLLGFQWQLPPPPQNGFMNGTIPVGAGEPLPH 420

[illegible]


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Db      61 shqcahcektfnrkdhlknhlqthdpnkmafgeecgkkyntmlgykrhlaalhaassgd 120
Qy     121 TCGVCTLELGSTEVLDDHLKSHAEKANQAPREKKYQCDHCDRCFYTRKDVRRHLVVHTG 180
Db     121 tcgvcalelgstevlldhlkahaeeekppsgtkekkhqcdhcercfytrkdvrhlvvhtg 180
Qy     181 CKDFLCQFCAQRFGRKDHltrhtkKTHSQELMQENMQAGDYQSNFQLIAPSTSFQIKVDP 240
Db     181 ckdflcqfcaqrfgkrkdhltrhtkKTHSQELMQESlqtgdllstfhtisp--sfqlkaaa 238
Qy     241 MPPFQLGAAPENGLDGGPLPEVHGLVLAAPPEAPQPMPPLEPLEPLEPLEPMQSLEP 300
Db     239 lppfplgasagnglasslpaevhsltlsppeqaagpmqpl----- 278
Qy     301 LQPLEPMQPLEPMQPLEPMQPLEPLEPLEPMQPLEPMQPLEPMQPMLEPMQPMQPMQPMQ 360
Db     279 ----- 278
Qy     361 MLPMQPMLEPMQPMQPMQPMLEPMPEPSFTLHPGVVPTSPPPPIILQEHKYNPVPTSYAPFVG 420
Db     279 -----peslaslhpsvsgsppp-plpnhkynttstsysplas 315
Qy     421 MPVKADGKAFCNVGFFEEFPLQEPQAPLKFNPCFEMPMEGFGKVTLSKELLVDAVNIAIP 480
Db     316 lplkadtkgfcnlslfedlplqepqspqklnpgfdlakgnagkvnlpkelpadavnltp 375
Qy     481 ASLEISSLLGFWQLPPPTPQNGFVNSTIPVGPGEPLPHRITCLA-QQQPPPLP----- 532
Db     376 asldlspllgfwqlpppatqntfgnstlalgpgeslphrlsclgqqqqepplamgtvslg 435
Qy     533 --PPPPPLP 538
Db     436 qlplppip 443

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